STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _/0/609,383β_

Source: _1Fw/b_

Date Processed by STIC: _9/27/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
   User Manual** - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *10/609,383B*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
        prevent "wrapping."

2____Invalid Line Length   The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
    Numbering   use **space characters**, instead.

4____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
        ensure your subsequent submission is saved in ASCII text.**

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
        each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
        residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
        previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
        the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
        Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
    (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
        (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
        (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
        This sequence is intentionally skipped
        Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
    (NEW RULES)   <210> sequence id number
        <400> sequence id number
        000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
        In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
    Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
        is Artificial Sequence. (see item 11 below)

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use
        of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
        Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
        explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
        Sequence Rules

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
        listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – STIC Systems Branch – 03/02/06

IFW16

RAW SEQUENCE LISTING   DATE: 09/27/2006
PATENT APPLICATION: US/10/609,383B   TIME: 15:13:28

Input Set : F:\synthetic.txt
Output Set: N:\CRF4\09272006\J609383B.raw

see pp 7-8, too

```
       1 <110> APPLICANT: Feldmann, Richard J.; Connectron Holding, Inc.
       3 <120> TITLE OF INVENTION: Synthetic Connectron
       5 <130> FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
C-->   7 <140> CURRENT APPLICATION NUMBER: US/10/609,383B
C-->   7 <141> CURRENT FILING DATE: 2003-07-01
       8 <150> PRIOR APPLICATION NUMBER: US 60/393,558 and US 09/866,925
      10 <160> NUMBER OF SEQ ID NOS: 34
      12 <170> SOFTWARE: Proprietary
      15 <210> SEQ ID NO: 1
      17 <211> LENGTH: 217
      18 <212> TYPE: DNA
      19 <213> ORGANISM: Saccharomyces cerevisiae complete genome.
      21 <220> FEATURE:
      22 <222> LOCATION: (12572)...(12788)
      23 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 36
      26 <400> SEQUENCE: 1
      27 gcactggtaa  caggtggtaa  tgaagaagta  atttcctgac  ttgttgttgt  actggtaaca      60
      28 ggtggtaatg  atgaagtaat  ttcctgactt  gttgttgtac  tggtaacagg  tggtaatgaa     120
      29 gaagtaattt  cctgacttgt  tgttgcactg  gtaacaggtg  gtaatgatga  agtaatttcc     180
      30 tgacttgttg  ttgtactggt  aacaggtggt  aatgatg                                217
      33 <210> SEQ ID NO: 2
      35 <211> LENGTH: 236
      36 <212> TYPE: DNA
      37 <213> ORGANISM: Saccharomyces cerevisiae complete genome.
      39 <220> FEATURE:
      40 <222> LOCATION: (12572)...(12807)
      41 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 39
      44 <400> SEQUENCE: 2
      45 gcactggtaa  caggtggtaa  tgaagaagta  atttcctgac  ttgttgttgt  actggtaaca      60
      46 ggtggtaatg  atgaagtaat  ttcctgactt  gttgttgtac  tggtaacagg  tggtaatgaa     120
      47 gaagtaattt  cctgacttgt  tgttgcactg  gtaacaggtg  gtaatgatga  agtaatttcc     180
      48 tgacttgttg  ttgtactggt  aacaggtggt  aatgatgaag  cagtttcctg  gcttgt         236
      51 <210> SEQ ID NO: 3
      53 <211> LENGTH: 166
      54 <212> TYPE: DNA
      55 <213> ORGANISM: Saccharomyces cerevisiae complete genome.
      57 <220> FEATURE:
      58 <222> LOCATION: (24863)...(25028)
      59 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 112
      62 <400> SEQUENCE: 3
      63 aatcaccaaa  gtctacatat  tcgtcttcat  cattaccacc  tgttaccagt  gcaacaacaa      60
      64 gtcaggaaat  tacttcttca  ttaccacctg  ttaccactac  aaaaacgagc  gaacaaacca     120
      65 ctttggttac  cgtgacatcc  tgcgaatctc  atgtgtgcac  tgaatc                     166
```

Does Not Comply — Corrected Diskette Needed

incorrect format

list as <150> 60/393,558
<151> 2002-07-05, followed by
<150> 09/866,925
<151> 2001-05-30
on line below

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 68 <210> SEQ ID NO: 4
 70 <211> LENGTH: 37
 71 <212> TYPE: DNA
 72 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.
 74 <220> FEATURE:
 75 <222> LOCATION: (4626130)...(4626166)
 76 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
4651a
 79 <400> SEQUENCE: 4
 80 tctgatgaca   aacgccaaac   tgcctgatgc   gctacgc                                    37
 83 <210> SEQ ID NO: 5
 85 <211> LENGTH: 54
 86 <212> TYPE: DNA
 87 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.
 89 <220> FEATURE:
 90 <222> LOCATION: (705150)...(705203)
 91 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
811a
 94 <400> SEQUENCE: 5
 95 tctgatgaca   aacgccaaac   tgcctgatgc   gctacgctta   tcaggcctac   gcag            54
 98 <210> SEQ ID NO: 6
100 <211> LENGTH: 36
101 <212> TYPE: DNA
102 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.
104 <220> FEATURE:
105 <222> LOCATION: (757718)...(757753)
106 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
975
109 <400> SEQUENCE: 6
110 ttacgcctga   tgcgctgcgc   ttatcaggcc   tacggg                                    36
113 <210> SEQ ID NO: 7
115 <211> LENGTH: 37
116 <212> TYPE: DNA
117 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.
119 <220> FEATURE:
120 <222> LOCATION: (4626130)...(4626166)
121 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
4651a
124 <400> SEQUENCE: 7
125 tctgatgaca   aacgccaaac   tgcctgatgc   gctacgc                                    37
128 <210> SEQ ID NO: 8
130 <211> LENGTH: 54
131 <212> TYPE: DNA
132 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.
134 <220> FEATURE:
135 <222> LOCATION: (698713)...(698766)
136 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
809
139 <400> SEQUENCE: 8
140 tctgatgaca   aacgccaaac   tgcctgatgc   gctacgctta   tcaggcctac   gcag            54
143 <210> SEQ ID NO: 9
145 <211> LENGTH: 36
146 <212> TYPE: DNA
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147 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.

```
    149 <220> FEATURE:
    150 <222> LOCATION: (757718)...(757753)
    151 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
975
    154 <400> SEQUENCE: 9
    155 ttacgcctga  tgcgctgcgc  ttatcaggcc  tacggg                                      36
    158 <210> SEQ ID NO: 10
    160 <211> LENGTH: 16
    161 <212> TYPE: DNA
    162 <213> ORGANISM: Saccharomyces cerevisiae complete genome - problem.
    164 <220> FEATURE:
    165 <222> LOCATION: (221330)...(221345)
    166 <223> OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber =
792a
    169 <400> SEQUENCE: 10
    170 tatatatatg  tcactg                                                             16
    173 <210> SEQ ID NO: 11
    175 <211> LENGTH: 16
    176 <212> TYPE: DNA
    177 <213> ORGANISM: Saccharomyces cerevisiae complete genome - problem.
    179 <220> FEATURE:
    180 <222> LOCATION: (221346)...(221361)
    181 <223> OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber =
793
    184 <400> SEQUENCE: 11
    185 tattgcatgc  tggatg                                                             16
    188 <210> SEQ ID NO: 12
    190 <211> LENGTH: 539
    191 <212> TYPE: DNA
    192 <213> ORGANISM: Saccharomyces cerevisiae complete genome - problem.
    194 <220> FEATURE:
    195 <222> LOCATION: (448454)...(448992)
    196 <223> OTHER INFORMATION: Chromosome = 5 Strand = positive ConnectronObjectNumber =
4749
    199 <400> SEQUENCE: 12
    200 tatatatatg  tcactgtatt  gcatgctgga  tggtgttaga  caaggccgta  gggacatata          60
    201 gcatctagga  agtaaccttg  tacgaaaata  ggcaatattt  cctgtttagg  cgattgtgac         120
    202 gcagatttta  gtccaacgat  ctagcgtcaa  ggaatttttt  tatagtggga  cattgcacca         180
    203 aggaagtaac  ttgatacgtc  gtgggtgaat  gggtctgttt  tcttattcgg  cggggtaata         240
    204 catttttggg  ggaagtttgt  ctgtctgacg  cgccatatgt  aggtacgcca  aaaagggctc         300
    205 ctctacttcg  aagcgcgagg  tcgtatacct  aataaggaaa  tgtaatttat  aacttttat          360
    206 tatattggtc  ttttcgagag  cggaacgtag  gtccatgttt  aaagtatcca  agagaatatc         420
    207 cacgaagcgg  ctgagcaacg  aacagaatcc  tggttctcct  cgactaagca  gatagttaag         480
    208 atactgtgca  ccatggaaat  tgaaaacgaa  agtacgtacc  gactacttta  tttttgcag          539
    210 <210> SEQ ID NO: 13
    212 <211> LENGTH: 158
    213 <212> TYPE: DNA
    214 <213> ORGANISM: Saccharomyces cerevisiae complete genome - problem.
    216 <220> FEATURE:
    217 <222> LOCATION: (24863)...(25028)
    218 <223> OTHER INFORMATION: Chromosome = 5 Strand = negative ConnectronObjectNumber =
4824a
    221 <400> SEQUENCE: 13
```

222 tatatatatg tcactgtatt gcatgctgga tggtgttaga caaggccgta gggacatata   60

```
223 gcatctagga  agtaaccttg  tacgaaaata  ggcaatattt  cctgtttagg  cgattgtgac        120
224 gcagatttta  gtccaacgat  ctagcgtcaa  ggaatttt                                  158
226 <210> SEQ ID NO: 14
228 <211> LENGTH: 134
229 <212> TYPE: DNA
230 <213> ORGANISM: Halobacterium sp. NRC-1 complete genome.
232 <220> FEATURE:
233 <222> LOCATION: (732401)...(732534)
234 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
6612
237 <400> SEQUENCE: 14
238 ttcatcacag  acgaggacga  gcgcggccaa  gtggggatcg  gcacactcat  cgtgttcatc         60
239 gcgatggtgc  tggtcgccgc  gatcgccgcc  ggcgtcctca  tcaacactgc  cggctacctc        120
240 caatccaagg  ggtc                                                              134
243 <210> SEQ ID NO: 15
245 <211> LENGTH: 193
246 <212> TYPE: DNA
247 <213> ORGANISM: Halobacterium sp. NRC-1 complete genome.
249 <220> FEATURE:
250 <222> LOCATION: (733018)...(733209)
251 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
6644a
254 <400> SEQUENCE: 15
255 gacgagcgcg  gtcaagtggg  gatcggcaca  ctcatcgtgt  tcatcgcgat  ggtgctggtc         60
256 gccgcgatcg  ccgccggcgt  cctcatcaac  accgccggct  acctccaatc  caaggggtcg        120
257 gcaaccggtg  aggaagcctc  cgcacaggtc  tccaaccgca  tcaacatcgt  ctccgcgtac        180
258 ggcaacgtca  aca                                                              193
261 <210> SEQ ID NO: 16
263 <211> LENGTH: 85
264 <212> TYPE: DNA
265 <213> ORGANISM: Halobacterium sp. NRC-1 complete genome.
267 <220> FEATURE:
268 <222> LOCATION: (773399)...(773483)
269 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
6852
272 <400> SEQUENCE: 16
273 gtggggatcg  gcacgctcat  cgtgttcatc  gcgatggtgc  tggtcgccgc  gatcgccgcc         60
274 ggcgtcctca  tcaacactgc  cggct                                                  85
277 <210> SEQ ID NO: 17
279 <211> LENGTH: 121
280 <212> TYPE: DNA
281 <213> ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
283 <220> FEATURE:
284 <222> LOCATION: (4832718)...(4832838)
285 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
53464
288 <400> SEQUENCE: 17
289 gccaacatcg  aggccctcaa  cagccgcacg  gtgaacatcg  gccagatcct  cgaagtgatc         60
290 aagggcatct  ccgagcagac  caacctgctc  gccctcaacg  ccgccatcga  agccgcgcgc        120
291 g                                                                            121
294 <210> SEQ ID NO: 18
296 <211> LENGTH: 194
297 <212> TYPE: DNA
```

RAW SEQUENCE LISTING   DATE: 09/27/2006
PATENT APPLICATION: US/10/609,383B   TIME: 15:13:28

        Input Set : **F:\synthetic.txt**
        Output Set: **N:\CRF4\09272006\J609383B.raw**

    298 <213> ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
    300 <220> FEATURE:
    301 <222> LOCATION: (4836528)...(4836720)
    302 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
53531
    305 <400> SEQUENCE: 18
    306 ggacggcaaa caggtggtcg agcagaccat ccgcgcgatg aacgagcttt ccgagaagat   60
    307 cagcgcctcc tgcgccaaca tcgaggccct caacagccgc acggtgaaca tcggccagat   120
    308 cctcgaagtg atcaagggca tctccgagca gaccaacctg ctcgccctca acgccgccat   180
    309 cgaagccgcg cgcg   194
    312 <210> SEQ ID NO: 19
    314 <211> LENGTH: 169
    315 <212> TYPE: DNA
    316 <213> ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
    318 <220> FEATURE:
    319 <222> LOCATION: (4838678)...(4838846)
    320 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
53549a
    323 <400> SEQUENCE: 19
    324 accatccgcg cgatgaacga gctttccgag aagatcagcg cctcctgcgc caacatcgag   60
    325 gccctcaaca gccgcacggt gaacatcggc cagatcctcg aagtgatcaa gggcatctcc   120
    326 gagcagacca acctgctcgc cctcaacgcc gccatcgaag ccgcgcgcg   169
    329 <210> SEQ ID NO: 20
    331 <211> LENGTH: 36
    332 <212> TYPE: DNA
    333 <213> ORGANISM: Sequence Recognized by Synthetic DNA Binding Protein.
    335 <220> FEATURE:
    338 <400> SEQUENCE: 20
    339 tccccatgag catagatatg caggtaggcg gcaagt
    342 <210> SEQ ID NO: 21
    344 <211> LENGTH: 136
    345 <212> TYPE: DNA
    346 <213> ORGANISM: Vibrio cholerae chromosome I, complete chromosome.
    348 <220> FEATURE:
    349 <222> LOCATION: (952641)...(952777)
    350 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
607
    353 <400> SEQUENCE: 21
    354 tgtatatacc caaactactt ggagttgcag gtaggcggca agtgagtgag tccccatgag   60
    355 catagataga ctatgtgatt ggggtgaacg aacgtagcca acaccgctgc agcttcaagt   120
    356 aggaagggta tacctt   136
    359 <210> SEQ ID NO: 22
    361 <211> LENGTH: 117
    362 <212> TYPE: DNA
    363 <213> ORGANISM: Vibrio cholerae chromosome I, complete chromosome.
    365 <220> FEATURE:
    366 <222> LOCATION: (1005810)...(1005926)
    367 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
646
    370 <400> SEQUENCE: 22
    371 taccaaaact acttggagtt gcaggtaggc ggcaagagag tgaatcccca tcagcataga   60
    372 cagactatgt gattggggtg aacgaacgta gccaataccg ctgcagcttc aagtagg   117
    375 <210> SEQ ID NO: 23

Invalid response. See item 10 on Error Summary Sheet.
also, if this is an artificial sequence, please give source of genetic material

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/27/2006
PATENT APPLICATION: US/10/609,383B   TIME: 15:13:29

Input Set : **F:\synthetic.txt**
Output Set: **N:\CRF4\09272006\J609383B.raw**

<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

```
Seq#:1; Line(s) 27,28,29,30
Seq#:2; Line(s) 45,46,47,48
Seq#:3; Line(s) 63,64,65
Seq#:4; Line(s) 76,80
Seq#:5; Line(s) 95
Seq#:6; Line(s) 110
Seq#:7; Line(s) 121,125
Seq#:8; Line(s) 140
Seq#:9; Line(s) 155
Seq#:10; Line(s) 170
Seq#:12; Line(s) 200,201,202,203,204,205,206,207,208
Seq#:13; Line(s) 222,223,224
Seq#:14; Line(s) 238,239,240
Seq#:15; Line(s) 255,256,257,258
Seq#:16; Line(s) 273,274
Seq#:17; Line(s) 289,290,291
Seq#:18; Line(s) 306,307,308,309
Seq#:19; Line(s) 324,325,326
Seq#:20; Line(s) 339
Seq#:21; Line(s) 354,355,356
Seq#:22; Line(s) 371,372
Seq#:23; Line(s) 385
Seq#:24; Line(s) 400,401,402
Seq#:25; Line(s) 417,418
Seq#:26; Line(s) 425,431
Seq#:27; Line(s) 438,444
Seq#:28; Line(s) 459,460
Seq#:29; Line(s) 475,476,477
Seq#:30; Line(s) 489
Seq#:31; Line(s) 500
Seq#:32; Line(s) 511
Seq#:33; Line(s) 522
Seq#:34; Line(s) 533
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VERIFICATION SUMMARY   DATE: 09/27/2006
PATENT APPLICATION: **US/10/609,383B**   TIME: 15:13:29

Input Set : **F:\synthetic.txt**
Output Set: **N:\CRF4\09272006\J609383B.raw**

L:7 M:270 C: Current Application Number differs, Missing <140> CURRENT APPLICATION NUMBER: is
Added.
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date